ANALYSIS OF *BRAF* (V600E) MUTATION AND *RET/PTC* REARRANGEMENTS IN THYROID CARCINOMAS

Loiola, S.O.[1], Levy, C.B. [1], Castro,V.R.M.[2], Basílio,C.A.[3], Henriques,J.M.M.[2], Oliveira, P.M.F.[2], De Moura Gallo, C.V[1]

[1]Departamento de Biologia Celular e Genética, Instituto de Biologia,UERJ, Rio de Janeiro, Brasil; [2]Disciplina de Endocrinologia, Faculdade de Ciências Médicas, UERJ, Rio de Janeiro, Brasil; [3] Laboratório de Anatomia Patológica do Hospital Gaffrée e Guinle-UNI-RIO, Rio de Janeiro, Brasil

Thyroid nodules are very frequent, however only 5% are malignant. More than 95% of thyroid carcinomas are derived from follicular cells. Follicular-cell-derived carcinomas are divided into well-differentiated, poorly differentiated and undifferentiated types on the basis of histological and clinical parameters. Papillary thyroid carcinoma (PTC) is the most common thyroid carcinoma. Recent advances have improved knowledge of its pathogenesis; these include the identification of genetic alterations that activate a common effector pathway involving the RET–Ras–BRAF signalling cascade. In order to better understand the process of thyroid tumorigenesis in malignant tumors we studied the presence of *BRAF* V600E mutation and *RET/PTC$_1$* and *RET/PTC$_3$* rearrangements in thyroid tumors, including papillary and anaplastic carcinomas. The specimens were obtained from surgical and fine-needle aspiration biopsies. In the classical PTC analyzed we found the 31.6 % *BRAF* V600E mutation. The rearrangement *RET/PTC$_1$* was present in 23.5% and *RET/PTC$_3$* in 35.4% of the malignant tumors analyzed. These data can provide powerful diagnostic tools and can also be used to identify new therapeutic targets.

Supported by: FAPERJ, UERJ.